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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 23:06:16 ; Search time 2773 Seconds

(without alignments)
5982.185 Million cell updates/sec

Title: US-09-895-298A-32_COPY_63_632

Perfect score: 570

Sequence: 1 atgatgaattccagctcc.....aagaaggtatccaagggcc 570

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	568.4	99.7	1219	6	AX108540	AX108540 Sequence
2	568.4	99.7	1813	9	AK023655	AK023655 Homo sapi
3	568.4	99.7	1960	6	AX108538	AX108538 Sequence
4	568.4	99.7	2407	6	AX108534	AX108534 Sequence
5	568.4	99.7	2521	6	AX108536	AX108536 Sequence
6	568.4	99.7	2760	9	BC027602	BC027602 Homo sapi
7	565.2	99.2	2387	9	AK093944	AK093944 Homo sapi
8	377.4	66.2	2399	9	AK097718	AK097718 Homo sapi
9	176	30.9	220633	9	HU091321	U91321 Human Chrom
10	176	30.9	223280	2	AC130456	AC130456 Homo sapi
11	141	24.7	71596	2	AC100877	AC100877 Mus muscu
12	127.2	22.3	402	6	AX071021	AX071021 Sequence
13	106.2	18.6	110000	2	AC124444_2	Continuation (3 of
14	105.4	18.5	164564	9	HUAC003108	AC003108 Human Chr
15	100.4	17.6	1639	9	AB002405	AB002405 Homo sapi
16	100.4	17.6	1804	9	BC018346	BC018346 Homo sapi
17	100.4	17.6	5291	9	AK074065	AK074065 Homo sapi
18	90.8	15.9	1658	10	BC013502	BC013502 Mus muscu
19	90.8	15.9	2848	10	BC004840	BC004840 Mus muscu
20	84.8	14.9	623	10	MMU297000	AJ297000 Mus muscu
21	71.8	12.6	81704	9	AL512353	AL512353 Human DNA
22	71.8	12.6	192180	2	AC023331	AC023331 Homo sapi
23	61	10.7	1983	10	BC005510	BC005510 Mus muscu
24	61	10.7	2614	10	BC006956	BC006956 Mus muscu
25	60.4	10.6	71596	2	AC100877	AC100877 Mus muscu
26	53.2	9.3	7218	6	166494	166494 Sequence 14
27	49.4	8.7	37026	9	CNS00YVF	AL096808 Homo sapi
28	48.4	8.5	256745	2	AL772305	AL772305 Mus muscu
29	47.8	8.4	177738	9	AC021593	AC021593 Homo sapi
30	47.6	8.4	193465	2	AL645856	AL645856 Mus muscu
31	43.8	7.7	144003	2	AC113536	AC113536 Mus muscu
32	42.6	7.5	7218	6	166494	166494 Sequence 14
33	42.6	7.5	195221	2	AC099288	AC099288 Rattus no
34	42.6	7.5	217374	2	AC106531	AC106531 Rattus no
35	42	7.4	170013	2	AC128188	AC128188 Rattus no
36	41.8	7.3	174313	2	AC117017	AC117017 Rattus no
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38	41	7.2	116408	2	AC129743	AC129743 Rattus no
39	41	7.2	180331	2	RN105N20	AL603728 Rattus no
40	40.8	7.2	198826	2	AL845547	AL845547 Mus muscu
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44	40.2	7.1	122855	3	AC084159	AC084159 Caenorhab
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ALIGNMENTS

RESULT 1	AX108540	1219 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX108540	Sequence 7 from Patent WO0123417.			
DEFINITION	AX108540				
ACCESSION	AX108540.1	GI:13923839			
VERSION					
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1 (bases 1 to 1219)				
	vinals y de Bassols, C.				
	Human tumor-associated lak-4p related polynucleotides and				
	polypeptides and their uses				

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0123417-A 7 05-APR-2001;

SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)

FEATURES

Source

Location/Qualifiers
1. .1219

BASE COUNT	346 a	260 c	275 g	338 t
ORIGIN				

Query Match	99.78;	Score 568.4;	DB 6;	Length 1219;
Best Local Similarity	99.88;	Pred. No. 2e-147;		
Matches 569; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	ATGATGAATTTCCAGCCCTCCGAGCAAAAGCCTGGGGGGCCCTACAGATGATGACTTTCTTC	60
Db	4	ATGATGAATTTCCAGCCCTCCGAGCAAAAGCCTGGGGGGCCCTACAGATGATGACTTTCTTC	63
QY	61	ATCTTTCTGCTCTTTTTCCTTCATCTTTCAACCGGGGCTTTGTCACCCCTGGCCATCACCATC	120
Db	64	ATCTTTCTGCTCTTTTTCCTTCATCTTTTCACCGGGGCTTTGTCACCCCTGGCCATCACCATC	123
QY	121	TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGTCTGCTCTCTTCATTTCAC	180
Db	124	TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGTCTGCTCTCTTCATTTCAC	183
QY	181	TCCATCTACAGCTGGATCGACACACCCTAAGTACACGGCCCTGCTACCTGTGGTGTGTTGG	240
Db	184	TCCATCTACAGCTGGATCGACACACCCTAAGTACACGGCCCTGCTACCTGTGGTGTGTTGG	243
QY	241	ATCTATCGGAACCTCATTTGGAAGTGTGTACACTTTTTCATCTCACCCTCATTTGTGCTA	300
Db	244	ATCTATCGGAACCTCATTTGGAAGTGTGTACACTTTTTCATCTCACCCTCATTTGTGCTG	303
QY	301	ATCATCACCTATCTTTTACTTGGCAGATTCACAGAGGGGAAGAGATTATGATTAAGCTGTGCTC	360
Db	304	ATCATCACCTATCTTTTACTTGGCAGATTCACAGAGGGGAAGAGATTATGATTAAGCTGTGCTC	363
QY	361	CATGAGCAGATCATTTAATGAGGGGCAAAAGATAAATGTTCCTGATAGAAAAATTGATCAAG	420
Db	364	CATGAGCAGATCATTTAATGAGGGGCAAAAGATAAATGTTCCTGATAGAAAAATTGATCAAG	423
QY	421	CTGCAGGATATGAGAAAGAAAGCAAAACCCAGCTTCACCTTGTCTGGAAGGAGAGAGGTG	480
Db	424	CTGCAGGATATGAGAAAGAAAGCAAAACCCAGCTTCACCTTGTCTGGAAGGAGAGAGGTG	483
QY	481	GAGCAACAAGGCTTTTTCGATTTTGGGGGAACATGATGGCAGTCTTGACTTGGCATCTAGA	540
Db	484	GAGCAACAAGGCTTTTTCGATTTTGGGGGAACATGATGGCAGTCTTGACTTGGCATCTAGA	543
QY	541	AGATCAGTTCAAGAAGGTAATCCAAAGGCC 570	
Db	544	AGATCAGTTCAAGAAGGTAATCCAAAGGCC 573	

RESULT 2
AK023655

LOCUS	AK023655	2013 bp	linear
DEFINITION	Homo sapiens cDNA FLJ13593 fs, clone PLACE1009493.		
ACCESSION	AK023655		
VERSION	AK023655.1	GI:10435644	
KEYWORDS	oligo capping; fts (full insert sequence).		
SOURCE	Homo sapiens placenta cDNA to mRNA, clone_1lb:PLACE1		

REFERENCE AUTHORS

Isojima, T., Ueda, Y., Hayashi, K., Sugiyama, T., Otsuna, Y., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakami, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakatsuki, A.,

TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1813)
AUTHORS Isogai, T. and Otsuki, T.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,

COMMENT

Genomics Laboratory: 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hrl.co.jp, Tel: 81-438-552-3975, Fax: 81-438-52-3986
NEDO human cDNA sequencing project supporting by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES	Location/Qualifiers
source	1. .1813

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/note="Cloning vector: pME18SFL3"
CDS      31..1023

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/translacion="MRLVERKEMPRHEVYVLLNRNIFLKISIIIGILCYUWNTVALS
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IFLLEFPSEFTGVLCTAITIMRLKPSADCGPFRCIPLFITSISYSDITLSTPGYLT
VMYIRNLIGSVHFFLITLIVLITLWQITTEGKIMIRLLHQIINEGKRMFL"
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Query Match	99.78;	Score 568.4;	DB 9;	Length 1813;
Best Local Similarity	99.88;	Pred. No. 2.1e-147;		
Matches 569;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps
QY 1	ATGATGAATTTCCAGCCCTCCGAGCAAAAGCCTGGCGGGCCCTACAGATGATGACTTTCCTTC	60		
Db 451	ATGATGAATTTCCAGCCCTCCGAGCAAAAGCCTGGCGGGCCCTACAGATGATGACTTTCCTTC	5100		
QY 61	ATCTCTTGCTCTTTTCCCATCTTTCACCGGGGCTTGTGCACCCCTGGCCATCACCATC	1200		
Db 511	ATCTCTTGCTCTTTTCCCATCTTTCACCGGGGCTTGTGCACCCCTGGCCATCACCATC	5700		
QY 121	TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTTCGAGGCTGTGCCCTCTCTTCAATTAC	1800		
Db 571	TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTTCGAGGCTGTGCCCTCTCTTCAATTAC	6300		
QY 181	TCCATCTACAGCTGGATGCGACACCCTAAGTACACGGCCCTGCTACCTGTGGTGTGTTGG	2400		
Db 631	TCCATCTACAGCTGGATGCGACACCCTAAGTACACGGCCCTGCTACCTGTGGTGTGTTGG	6900		
QY 241	ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTTGTGCTA	3000		
Db 691	ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTTGTGCTA	7500		
QY 301	ATCATCACCTATCTTTACTTGGCAGATTCACAGAGGGAAGGAATTATGATTAAGGCTGCTC	3600		
Db 751	ATCATCACCTATCTTTACTTGGCAGATTCACAGAGGGAAGGAATTATGATTAAGGCTGCTC	8100		
QY 361	CATGACGAGATTCATTAATGAGGGCAAGATAAATGTCTCGATAGAAAAATTGATCAAG	4200		
Db 811	CATGACGAGATTCATTAATGAGGGCAAGATAAATGTCTCGATAGAAAAATTGATCAAG	8700		
QY 421	CTGCAGGATATGGAGAAAGCAAAACCCACGCTCACCTGTCTTCGAAAGGAGAGAGGTG	4800		
Db 871	CTGCAGGATATGGAGAAAGCAAAACCCACGCTCACCTGTCTTCGAAAGGAGAGAGGTG	9300		

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QY 481 GAGCAACAAGGCTTTTGCAATTGGGGGAACATGATGCGAGTCTTGACTTGGCATCTAGA 540
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Db 931 GAGCAACAAGGCTTTTGCAATTGGGGGAACATGATGCGAGTCTTGACTTGGCATCTAGA 990

QY 541 AGATCAGTTCAGAAGGTAATCCAAGGGCC 570
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Db 991 AGATCAGTTCAGAAGGTAATCCAAGGGCC 1020

RESULT 3
AX108538 1960 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 5 from Patent WO0123417.
DEFINITION AX108538
ACCESSION AX108538
VERSION AX108538.1 GI:13923838
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 1960)
JOURNAL vinals y de Bassols,C.
REFERENCE Human tumor-associated lak-4p related polynucleotides and
AUTHORS polypeptides and their uses
TITLE Patent: WO 0123417-A 5 05-APR-2001;
JOURNAL SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES
source location/Qualifiers
1.1960
BASE COUNT /organism="Homo sapiens"
515 a 439 c 447 g 559 t /db_xref="taxon:9606"
ORIGIN

Query Match 99.7%; Score 568.4; DB 6; Length 1960;
Best Local Similarity 99.8%; Pred. No. 2.1e-147;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAATTCACAGCCTCCGAGAAAGCCTGGCGGCTCACAGATGATGACTTCTTC 60
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Db 805 ATCTTCTTGCTCTTTTCCCATCTTTCACCCGGGCTTGTGACACCTGGCCATCACCATC 864

QY 121 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCTCTCTTCATTAC 180
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Db 865 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCTCTCTTCATTAC 924

QY 181 TCCATCTACAGCTGGATGGACACACCTTAAGTACACGGGCTGGCTACCTGTGGGTGTTGG 240
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Db 925 TCCATCTACAGCTGGATGGACACACCTTAAGTACACGGGCTGGCTACCTGTGGGTGTTGG 984

QY 241 ATCTATCGGAACCTCATTTGGAAGTGTGCACCTCTTTTTCATCCTCACCCCTCATTTGTCTA 300
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Db 985 ATCTATCGGAACCTCATTTGGAAGTGTGCACCTCTTTTTCATCCTCACCCCTCATTTGTCTG 1044

QY 301 ATCATCACCTATCTTTACTGGCAGATCACAGAGGAAGGAAGATATATGTAAGGCTGCTC 360
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Db 1045 ATCATCACCTATCTTTACTGGCAGATCACAGAGGAAGGAAGATATATGTAAGGCTGCTC 1104

QY 361 CATGAGCAGATCATTAATGAGGGCAAAAGATAAATGTTCTTGATAGAAAATTTGATCAAG 420
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Db 1105 CATGAGCAGATCATTAATGAGGGCAAAAGATAAATGTTCTTGATAGAAAATTTGATCAAG 1164

QY 421 CTGAGGATATGAGAGAAAGCAAAACCCAGCTCAGCTTGTCTGGAAGAGAGAGAGGTG 480
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Db 1165 CTGAGGATATGAGAGAAAGCAAAACCCAGCTCAGCTTGTCTGGAAGAGAGAGAGGTG 1224

QY 481 GAGCAACAAGGCTTTTTCATTTGGGGGAACATGATGCGAGTCTTGACTTGGCATCTAGA 540
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QY 541 AGATCAGTTCAGAAGGTAATCCAAGGGCC 570
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RESULT 4
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LOCUS Sequence 1 from Patent WO0123417.
DEFINITION AX108534
ACCESSION AX108534
VERSION AX108534.1 GI:13923834
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 2407)
JOURNAL vinals y de Bassols,C.
REFERENCE Human tumor-associated lak-4p related polynucleotides and
AUTHORS polypeptides and their uses
TITLE Patent: WO 0123417-A 1 05-APR-2001;
JOURNAL SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES
source location/Qualifiers
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BASE COUNT /organism="Homo sapiens"
635 a 557 c 546 g 669 t /db_xref="taxon:9606"
ORIGIN

Query Match 99.7%; Score 568.4; DB 6; Length 2407;
Best Local Similarity 99.8%; Pred. No. 2.2e-147;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAATTCACAGCCTCCGAGAAAGCCTGGCGGCTCACAGATGATGACTTCTTC 60
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QY 61 ATCTTCTTGCTCTTTTCCCATCTTTCACCCGGGCTTGTGACACCTGGCCATCACCATC 120
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Db 1252 ATCTTCTTGCTCTTTTCCCATCTTTCACCCGGGCTTGTGACACCTGGCCATCACCATC 1311

QY 121 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTGCTGCCCTCTTCAATTCAC 180
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Db 1312 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTGCTGCCCTCTTCAATTCAC 1371

QY 181 TCCATCTACAGCTGGATGGACACACCTTAAGTACACGGGCTGGCTAACCTGTGGGTGTTGG 240
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Db 1372 TCCATCTACAGCTGGATGGACACACCTTAAGTACACGGGCTGGCTAACCTGTGGGTGTTGG 1431

QY 241 ATCTATCGGAACCTCATTTGGAAGTGTGCACCTCTTTTTCATCCTCACCCCTCATTTGTGCTA 300
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Db 1492 ATCATCACCTATCTTTACTGGCAGATCACAGAGGAAGGAAGATTAATGTAAGGCTGCTC 1551

QY 361 CATGAGCAGATCATTAATGAGGGCAAAAGATAAATGTTCTTGATAGAAAATTTGATCAAG 420
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RESULT 5
AX108536
LOCUS AX108536 2521 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 3 from Patent WO0123417.
ACCESSION AX108536
VERSION AX108536.1 GI:13923835
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 2521)
AUTHORS vinals y de Bassols,C.
TITLE Human tumor-associated lak-4p related polynucleotides and
polypeptides and their uses
JOURNAL Patent: WO 0123417-A 3 05-APR-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 662 a 583 c 583 g 693 t
ORIGIN
Query Match 99.7%; Score 568.4; DB 6; Length 2521;
Best Local Similarity 99.8%; Pred. No. 2.2e-147;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGATGAATTTCCAGCCTCCGAGCAAGCCTGGCGGCTCAGAGATGATGACTTTCTTC 60
Db 1306 ATGATGAATTTCCAGCCTCCGAGCAAGCCTGGCGGCTCAGAGATGATGACTTTCTTC 1365
QY 61 ATCTTCTGCTCTTTTCCATCTTTACCGGGGCTTTGTGACCCCTGGCCATCACCATC 120
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QY 481 GAGCAACAAGGCTTTTTCATTTGGGGGAACATGATGGCAGTCTTGACTTGCATCTAGA 540
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Db 1846 AGATCAGTTCAAGAAGTAAATCCAGGGCC 1875

RESULT 6
BC027602

LOCUS BC027602 2760 bp mRNA linear PRI 01-MAY-2002
DEFINITION Homo sapiens, similar to RIKEN cDNA 4932443L08 gene, clone
MGC:26648 IMAGE:4839111, mRNA, complete cds.
ACCESSION BC027602
VERSION BC027602.1 GI:20381190
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 2760)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadanesystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
Series: IRAC Plate: 34 Row: P Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: Genomescan gene
prediction, similarity but not identity to protein.
FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
/clone="MGC:26648 IMAGE:4839111"
/issue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"
213..2495
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LSTSDIDVIDSQTVSKRNDQGNQVLRSTSLNSMSQTLHSEMGIDTPGSSHEV
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LNSISRAYRSKNSLSLINSISIMOKTLKIGKFGTSVLSYFNLRLWLFENISF
ILNFSFIIPQFTYVAKKNTLOFTGLEFTTGVGTRDTVMYGYFTNSTIQHNSGASY
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RNIFLKISIIIGILCYWLNTVALSGEECEWTLIGODIYRLMLDFEVLNVEFLGEFL
RRIIGMOLITSLGLEFDIARVLELIYAQTLWIGIFRPLPLPTOMIMLFIMFYK
NISLMNFPQPSKAMRASOMTFEFLFEPSPGVLCITAITIWLKPSADCGPFRG
LPLEFHSIYSWIDTISTRPGYLVWVWYIRNLIGSVHFFILTLIVITLYLWQITEG
RKIMIRLHEQIINEGDKMFLIEKLKLDMEKRNAPSSLVLERVEVQDFLHLGE
HDSGLDRSRVSVOGNPRA"
BASE COUNT 739 a 637 c 625 g 759 t
ORIGIN
Query Match 99.7%; Score 568.4; DB 9; Length 2760;
Best Local Similarity 99.8%; Pred. No. 2.2e-147;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGATGAATTTCCAGCCTCCGAGCAAGCCTGGCGGCTCAGAGATGATGACTTTCTTC 60

Db 1923 ATGATGAATTTCAGCCCTCCGAGCAAAAGCCTGGCGGCTCAGAGATGACTTCTTC 1982

QY 61 ATCTTCTGCTCTTTTCCCATCTTTCCACCGGGCTTTGTGACCCCTGGCCATCACCATC 120
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Db 1983 ATCTTCTGCTCTTTTCCCATCTTTCCACCGGGCTTTGTGACCCCTGGCCATCACCATC 2042
|||||

QY 121 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCTCTTCATTTCAC 180
|||||

Db 2043 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCTCTTCATTTCAC 2102
|||||

QY 181 TCCATCTACAGCTGGATGACACCCCTAAGTACAGCGCCTGGCTACCTGTGGTGTGG 240
|||||

Db 2103 TCCATCTACAGCTGGATGACACCCCTAAGTACAGCGCCTGGCTACCTGTGGTGTGG 2162
|||||

QY 241 ATCTATCGGAACCTCATTTGGAAGTGTGACCTCTTTTCATCCTCACCCCTCATTTGTGCTA 300
|||||

Db 2163 ATCTATCGGAACCTCATTTGGAAGTGTGACCTCTTTTCATCCTCACCCCTCATTTGTGCTA 2222
|||||

QY 301 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATTAAGGCTGCTC 360
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Db 2223 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATTAAGGCTGCTC 2282
|||||

QY 361 CATGACGAGATCATTAATGAGGGCAAAAGATTAATGTTCTCTGATAGAAAAATTGATCAAG 420
|||||

Db 2283 CATGACGAGATCATTAATGAGGGCAAAAGATTAATGTTCTCTGATAGAAAAATTGATCAAG 2342
|||||

QY 421 CTGACGAGATTGAGAGAAAGCAAAACCCAGCTCAGCTGTTCTGTGAAAAGAGAGAGGTG 480
|||||

Db 2343 CTGACGAGATTGAGAGAAAGCAAAACCCAGCTCAGCTGTTCTGTGAAAAGAGAGAGGTG 2402
|||||

QY 481 GAGCAACAAGGCTTTTTCGATTTGGGGGAACATGATGGCAGCTGTGACTTGGCATGTAGA 540
|||||

Db 2403 GAGCAACAAGGCTTTTTCGATTTGGGGGAACATGATGGCAGCTGTGACTTGGCATGTAGA 2462
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QY 541 AGATCAGTTCAAGAAGGTAATCCAAAGGCC 570
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Db 2463 AGATCAGTTCAAGAAGGTAATCCAAAGGCC 2492
|||||

RESULT 7
AK093944
LOCUS AK093944 2387 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ36625 f1s, clone TRACH2017368, weakly similar
to Homo sapiens mRNA for LAK-4p.
ACCESSION AK093944
VERSION AK093944.1 GI:21752906
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens trachea cDNA to mRNA, clone_lib:TRACH2
clone:TRACH2017368.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1
Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,
Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,
Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H.,
Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E.,
Katooka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,
Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T.,
Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuno, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
TITLE Unpublished
JOURNAL 2 (bases 1 to 2387)
REFERENCE Isogai, T. and Yamamoto, J.
AUTHORS Direct Submission
TITLE Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
JOURNAL kazusa-Kamatari, Kizatazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
source 1..2387
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TRACH2017368"
/tissue_type="trachea"
/clone_lib="TRACH2"
/note="cloning vector: pME18SFL3"
BASE COUNT 624 a 549 c 543 g 671 t
ORIGIN
Query Match 99.2%; Score 565.2; DB 9; Length 2387;
Best Local Similarity 99.5%; Pred. No. 1.7e-146;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGATGAATTTCCAGCCTCCGAGCAAAAGCCTGGCGGCTCAGAGATGACTTCTTC 60
|||||
Db 1025 ATGATGAATTTCCAGCCTCCGAGCAAAAGCCTGGCGGCTCAGAGATGACTTCTTC 1084
|||||

QY 61 ATCTTCTGCTCTTTTCCCATCTTTCCACCGGGCTTTGTGACCCCTGGCCATCACCATC 120
|||||

Db 1085 ATCTTCTGCTCTTTTCCCATCTTTCCACCGGGCTTTGTGACCCCTGGCCATCACCATC 1144
|||||

QY 121 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCTCTTCATTTCAC 180
|||||

Db 1145 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCTCTTCATTTCAC 1204
|||||

QY 181 TCCATCTACAGCTGGATGACACACCCCTAAGTACAGCGCCTGGCTACCTGTGGTGTGG 240
|||||

Db 1205 TCCATCTACAGCTGGATGACACACCCCTAAGTACAGCGCCTGGCTACCTGTGGTGTGG 1264
|||||

QY 241 ATCTATCGGAACCTCATTTGGAAGTGTGACCTCTTTTCATCCTCACCCCTATTGTGCTA 300
|||||

Db 1265 ATCTATCGGAACCTCATTTGGAAGTGTGACCTCTTTTCATCCTCACCCCTATTGTGCTA 1324
|||||

QY 301 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATTAAGGCTGCTC 360
|||||

Db 1325 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATTAAGGCTGCTC 1384
|||||

QY 361 CATGACGAGATCATTAATGAGGGCAAAAGATTAATGTTCTCTGATAGAAAAATTGATCAAG 420
|||||

Db 1385 CATGACGAGATCATTAATGAGGGCAAAAGATTAATGTTCTCTGATAGAAAAATTGATCAAG 1444
|||||

QY 421 CTGACGAGATATGAGAGAAAGCAAAACCCAGCTCAGCTGTTCTGTGAAAAGAGAGAGGTG 480
|||||

Db 1445 CTGACGAGATATGAGAGAAAGCAAAACCCAGCTCAGCTGTTCTGTGAAAAGAGAGAGGTG 1504
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QY 481 GAGCAACAAGGCTTTTTCGATTTGGGGGAACATGATGGCAGCTGTGACTTGGCATGTAGA 540
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Db 1505 GAGCAACAAGGCTTTTTCGATTTGGGGGAACATGATGGCAGCTGTGACTTGGCATGTAGA 1564
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QY 541 AGATCAGTTCAAGAAGGTAATCCAAAGGCC 570
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Db 1565 AGATCAGTTCAAGAAGGTAATCCAAAGGCC 1594
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RESULT 8
AK097718
LOCUS AK097718 2399 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ40399 f1s, clone TESTR12037081, weakly similar
to Homo sapiens mRNA for LAK-4p.
ACCESSION AK097718
VERSION AK097718.1 GI:21757573
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens testis cDNA to mRNA, clone_lib:TESTR12


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clone:TEST12037081.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,
Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B.,
Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and
Isogai, T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2399)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
Source
1. 2399
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TEST12037081"
/tissue_type="testis"
/clone_id="TEST12"
/note="cloning vector: PME18SFL3"
BASE COUNT 610 a 591 c 528 g 670 t
ORIGIN
Query Match 66.2%; Score 377.4; DB 9; Length 2399;
Best Local Similarity 99.7%; Pred. No. 4e-94;
Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGATGAATTCCAGCCTCCGAGCAAGCCTGGCGGCTCCACAGATGATGACTTTCTTC 60
Db 1933 ATGATGAATTCCAGCCTCCGAGCAAGCCTGGCGGCTCCACAGATGATGACTTTCTTC 1992
QY 61 ATCTTCTGCTCTTTTCCCATCTTTCACCGGGGCTTGTGACACCTGGCCATCACCATC 120
Db 1993 ATCTTCTGCTCTTTTCCCATCTTTCACCGGGGCTTGTGACACCTGGCCATCACCATC 2052
QY 121 TGGAGATTGAAGCCTTCAGCTGAGCTGGCCCTTTTCGAGTCTGCCTCTTCATTAC 180
Db 2053 TGGAGATTGAAGCCTTCAGCTGAGCTGGCCCTTTTCGAGTCTGCCTCTTCATTAC 2112
QY 181 TCCATCTACAGCTGATGACACCCCTAAGTACACGGCTGCTACCTGTGGGTGTTGG 240
Db 2113 TCCATCTACAGCTGATGACACCCCTAAGTACACGGCTGCTACCTGTGGGTGTTGG 2172
QY 241 ATCTATGGAACCTCATTTGGAAGTGTGACCTTTTTCATCTCACCCTCATTTGTGCTA 300
Db 2173 ATCTATGGAACCTCATTTGGAAGTGTGACCTTTTTCATCTCACCCTCATTTGTGCTA 2232
QY 301 ATCATCACCATTCTTTACTGGCAGATCAGAGGAAGAGATTATGATAGGCTGCTC 360
Db 2233 ATCATCACCATTCTTTACTGGCAGATCAGAGGAAGAGATTATGATAGGCTGCTC 2292
QY 361 CATGAGCAGATCATTAATG 379
Db 2293 CATGAGCAGATCATTAATG 2311

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RESULT 9
HUU91321 LOCUS 220633 bp DNA linear PRI 10-JAN-2000
DEFINITION Human Chromosome 16 BAC clone CTR9875R-A-363E6, complete sequence.
ACCESSION U91321
VERSION U91321.1 GI:2951946
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 220633)
AUTHORS Loftus, B.J., Kim, U.J., Sneddon, V.P., Kalush, F., Brandon, R.,
Fuhrmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L.,
Deslattes, Mays, A., Cao, Y., Xu, R.X., Kang, H.L., Mitchell, S.,
Eichler, E.E., Harris, P.C., Venter, J.C. and Adams, M.D.
TITLE Genome duplications and other features in 12 Mb of DNA sequence
from human chromosome 16p and 16q
JOURNAL Genomics 60 (3), 295-308 (1999)
MEDLINE 99425270
PUBMED 10493829
REFERENCE 2 (bases 1 to 220633)
AUTHORS Adams, M.D., Loftus, B.J., Phillips, C.A., Zhou, L., Brandon, R.,
Fuhrmann, J. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-1997) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 220633)
REFERENCE Adams, M.D., Loftus, B.J., Zhou, L. and Labombard, M.
AUTHORS Direct Submission
JOURNAL Submitted (21-MAY-1997)
4 (bases 1 to 220633)
REFERENCE Adams, M.D., Loftus, B.J., Zhou, L., La Bombard, M., Kim, U.J. and
AUTHORS Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (19-AUG-1997) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
5 (bases 1 to 220633)
REFERENCE Adams, M.D., Loftus, B.J., Zhou, L., La Bombard, M., Kim, U.J. and
AUTHORS Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-1997) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
6 (bases 1 to 220633)
REFERENCE Adams, M.D.
AUTHORS Direct Submission
JOURNAL Submitted (11-MAR-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
COMMENT On Mar 11, 1998 this sequence version replaced gi:2335062.
BAC clone CTR9875R-A-363E6 is located in band 16p13.1 of chromosome
16. Genes were identified by a combination of five methods:
XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov),
GeneFinder (available by anonymous ftp from
colin@u.washington.edu), GENSCAN (available using the e-mail server
at gencodegenomic.stanford.edu), searches of the EST database at
TIGR (http://www.tigr.org/tdb/hcd/hcd.html) and searches against a
peptide database. Repeats were identified using RepeatMasker (Smit,
A.F.A. and Green, P. unpublished,
http://ftp.genome.washington.edu/rm/RepeatMasker.html).
FEATURES
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/complement(82033..108338)
/gene="363E6.1"
/complement(join(82033..82152,82283..82349,107848..108338))
/gene="363E6.1"
/complement(join(82117..82152,82283..82349,107848..107915))
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/product="Unknown gene product"
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/translation="MPTRPQPPVPRFLTSSQERIHRCRRLSPDAGLVILDFPASR
TIMAPSAWFLF"
complement(217478..219568)
/gene="363E6.2"
complement(join(217478..218093,219357..219568))
/gene="363E6.2"
complement(join(217946..218093,219357..219568))
/gene="363E6.2"
/codon_start=1
/product="Unknown gene product"
/protein_id="AAC05440.1"
/db_xref="GI:2951948"
/translation="MROTDRDVIPTALTRPMSLSHTGDKPRYDTEFMKHFVMMDL
LDMSMINILWYLCGISAPFLMQKDEVSPLYLKKWSAKGIQVGVMTVTFDEKSYESH
GSSYITDSMVEDECPHF"
BASE COUNT 61048 a 48977 c 49108 g 61449 t 51 others
ORIGIN

Query Match 30.9%; Score 176; DB 9; Length 220633;
Best Local Similarity 100.0%; Pred. No. 1e-37;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 AGATTGAAGCCTTCAGCTGACGTGGCCCTTTTCGAGGTGCTCTCTCATTCACCTCC 183
Db 204866 AGATTGAAGCCTTCAGCTGACGTGGCCCTTTTCGAGGTGCTCTCTCATTCACCTCC 204925

QY 184 ATCTACAGCTGATCGACACCCCTAAGTACACGGCCTGCTACCTGTGGGTGTTGGATC 243
Db 204926 ATCTACAGCTGATCGACACCCCTAAGTACACGGCCTGCTACCTGTGGGTGTTGGATC 204985

QY 244 TATCGAACCCTCATTTGGAAGTGTGCACCTCTTTTCATCCCTCACCCTCATTTGTGCT 299
Db 204986 TATCGAACCCTCATTTGGAAGTGTGCACCTCTTTTCATCCCTCACCCTCATTTGTGCT 205041

RESULT 10
AC130456 223280 bp DNA linear HTG 10-AUG-2002
LOCUS Homo sapiens chromosome 16 clone CTA-363E6, WORKING DRAFT SEQUENCE,
AC130456 5 unordered pieces.
AC130456
AC130456.1 GI:22203229
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 223280)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 223280)
JOURNAL DOE Joint Genome Institute.
REFERENCE Submitted (10-AUG-2002) Production Sequencing Facility, DOE Joint
TITLE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
JOURNAL -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 2773242
Center clone name: CIT978SKA_363E6
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Summary Statistics
Consensus quality: 221100 bases at least Q40
Consensus quality: 222027 bases at least Q30
Consensus quality: 222494 bases at least Q20
Estimated insert size: 220633; agarose-1p estimation
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Estimated insert size: 222880; sum-of-contigs estimation
Quality coverage: 10.81 in Q20 bases; agarose-1p estimation
Quality coverage: 10.71 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1261: contig of 1261 bp in length
* 1262 1361: gap of unknown length
* 1362 2690: contig of 1329 bp in length
* 2691 2790: gap of unknown length
* 2791 32134: contig of 29344 bp in length
* 32135 32235: gap of unknown length
* 32235 102578: contig of 70344 bp in length
* 102579 102678: gap of unknown length
* 102679 223280: contig of 120602 bp in length.
FEATURES
source location/Qualifiers
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/oranism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="CTA-363E6"
/clone_lib="CalTech human BAC library A"
BASE COUNT 61286 a 49953 c 49351 g 62289 t 401 others
ORIGIN

Query Match 30.9%; Score 176; DB 2; Length 223280;
Best Local Similarity 100.0%; Pred. No. 1e-37;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 AGATTGAAGCCTTCAGCTGACGTGGCCCTTTTCGAGGTGCTCTCTCATTCACCTCC 183
Db 86822 AGATTGAAGCCTTCAGCTGACGTGGCCCTTTTCGAGGTGCTCTCTCATTCACCTCC 86881

QY 184 ATCTACAGCTGATCGACACCCCTAAGTACACGGCCTGCTACCTGTGGGTGTTGGATC 243
Db 86882 ATCTACAGCTGATCGACACCCCTAAGTACACGGCCTGCTACCTGTGGGTGTTGGATC 86941

QY 244 TATCGAACCCTCATTTGGAAGTGTGCACCTCTTTTCATCCCTCACCCTCATTTGTGCT 299
Db 86942 TATCGAACCCTCATTTGGAAGTGTGCACCTCTTTTCATCCCTCACCCTCATTTGTGCT 86997

RESULT 11
AC100877 71596 bp DNA linear HTG 23-NOV-2001
LOCUS Mus musculus clone RP23-35B17, LOW-PASS SEQUENCE SAMPLING.
AC100877
AC100877.1 GI:17059651
VERSION HTG; HTGS_PHASE0.
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 71596)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-35B17
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 71596)
JOURNAL Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarato,J., Campiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kelis,C., Labocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
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TITLE
JOURNAL

COMMENT

Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., MCPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Rella,R., Ribick,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L13918
Center clone name: 35_B_17

* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 722: contig of 722 bp in length
* 723 822: gap of 100 bp
* 823 1526: contig of 704 bp in length
* 1527 1626: gap of 100 bp
* 1627 2336: contig of 710 bp in length
* 2337 2436: gap of 100 bp
* 2437 3156: contig of 720 bp in length
* 3157 3256: gap of 100 bp
* 3257 3984: contig of 728 bp in length
* 3985 4084: gap of 100 bp
* 4085 4811: contig of 727 bp in length
* 4812 4911: gap of 100 bp
* 4912 5638: contig of 727 bp in length
* 5639 5738: gap of 100 bp
* 5739 6477: contig of 739 bp in length
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* 6578 7305: contig of 728 bp in length
* 7306 7405: gap of 100 bp
* 7406 8107: contig of 702 bp in length
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* 8951 9050: gap of 100 bp
* 9051 9743: contig of 693 bp in length
* 9744 9843: gap of 100 bp
* 9844 10583: contig of 740 bp in length
* 10584 10683: gap of 100 bp
* 10684 11405: contig of 722 bp in length
* 11406 11505: gap of 100 bp
* 11506 12236: contig of 731 bp in length
* 12237 12336: gap of 100 bp
* 12337 13069: contig of 733 bp in length
* 13070 13169: gap of 100 bp
* 13170 13851: contig of 682 bp in length
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* 13952 14685: contig of 734 bp in length

14686 14785: gap of 100 bp
* 14786 15512: contig of 727 bp in length
* 15513 15612: gap of 100 bp
* 15613 16342: contig of 730 bp in length
* 16343 16442: gap of 100 bp
* 16443 17175: contig of 733 bp in length
* 17176 17275: gap of 100 bp
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* 17974 18073: gap of 100 bp
* 18074 18798: contig of 725 bp in length
* 18799 18898: gap of 100 bp
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* 29421 29520: gap of 100 bp
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* 30247 30346: gap of 100 bp
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* 34507 35237: contig of 731 bp in length
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* 36166 36880: contig of 715 bp in length
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* 41013 41112: gap of 100 bp
* 41113 41852: contig of 740 bp in length
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*	46909	47613:	contig of 705 bp	in length
*	47614	47713:	gap of 100 bp	
*	47714	48431:	contig of 718 bp	in length
*	48432	48531:	gap of 100 bp	
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*	49281	49380:	gap of 100 bp	
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*	50240	50966:	contig of 727 bp	in length
*	50967	51066:	gap of 100 bp	
*	51067	51797:	contig of 731 bp	in length
*	51798	51897:	gap of 100 bp	
*	51898	52632:	contig of 735 bp	in length
*	52633	52732:	gap of 100 bp	
*	52733	53448:	contig of 716 bp	in length
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*	53549	54266:	contig of 718 bp	in length
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*	54367	55107:	contig of 741 bp	in length
*	55108	55207:	gap of 100 bp	
*	55208	55927:	contig of 720 bp	in length
*	55928	56027:	gap of 100 bp	
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Query Match	24.7%;	Score 141;	DB 2;	Length 71596;
Best Local Similarity	86.2%;	Pred. No. 5e-28;		
Matches 156;	Conservative 0;	Mismatches 25;	Indels 0;	Gaps 0;

QY	119	TCTGGAGATTGAAGCCTTCACGCTGACTGTGGCCCTTTTTCGAGGTCGTGCCCTCTCTCATTC	178
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QY	179	ACTCCATCTACAGCTGGATGCACACCCTTAAGTAGACGGCCCTGGCTAACCTGTGGGTTGTTTT	238
Dd	48712	AATCCATCTACAGCTGSATTGACACCTCGAAGCCGACGGCTGGCTACCTGTGGGTCGCTCT	48771
QY	239	GGAATCTATCGGAACCTCATTTGGAAAGTGTGCACCTCTTTTCATCCACCCCATTTGTGC	298
Dd	48772	GGATCTACCAAGAATCTCATTTGGAAAGTGTGCACCTCTTTTCATCCACCCCATTTGTGC	48831
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Dd	48832	T 48832	

RESULT	12
LOCUS	AX071021
DEFINITION	AX071021
ACCESSION	AX071021
VERSION	AX071021.1
KEYWORDS	GI:12581294
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 402)
AUTHORS	Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J., Kssam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D., Lamson,G., Drmanac,R., Crtjenjakov,R., Drmanac,S., Dickson,M., Iabat,I., Leshkowitz,D., Kita,D., Garcia,Y. and Strache-Crain,B. Human genes and gene expression products Patent: WO 0102568-A 1493 11-JAN-2001;
TITLE	CHIRON CORPORATION (US) ; HYSEQ, INC. (US)
JOURNAL	Location/Qualifiers
FEATURES	1..402

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misc_feature /note="n = A,T,C or G"
BASE COUNT 83 a 106 c 87 g 124 t 2 others
ORIGIN

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Best Local Similarity	97.08;	Pred. No. 1.9e-24;		
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Db 269 ATGATGAAATTTCCAGCCTCCGAGCAAAAGCCTGGCGGGCCCTACAGATGAGGACTTTCTTC 328
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QY 61 AACTTCTGCTCTTTTTCACATCTTTCACCGGGGCTTGTGCACCCCTGGCCATCACCATC 120
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Db 329 AACTTCTGCTCTTTTTCACATCCTTTCACCGGGGCTTGTGCACCCCTGGCCATCACCATC 388
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QY 121 TCGAGATTTGAAGC 133
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Db 389 TTGAGATTTGAAGC 401

RESULT 13
AC124444_2/C
WPCOMMENT

Sequence split into 5 fragments LOCUS AC124444 Accession AC124444

FragmentName	Begin	End
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AC124444_1	100001	210000
AC124444_2	200001	310000
AC124444_3	300001	410000
AC124444_4	400001	410492

Query Match	18.6%;	Score 106.2;	DB 2;	Length 110000;
Best Local Similarity	86.7%;	Pred. No. 2.7e-18;		
Matches 117; Conservative	0;	Mismatches 18;	Indels 0;	Gaps 0;

QY	1	ATGATGAATTTTCCAGCCTCCGAGCAAAAGCCTGGCGGGCCCTACAGATGATGACTTCTTC	60
Db	84750	ATGATGAACCTTCCAGCCCCCAAGCAAGGCGCTGGCGGGCCCTACAGATGATTAACCTTCTTC	84631
QY	61	ATCTTCTTGCCTCTTTTTCACATCTTTACACGGGGTCTTGTGCACCCCTGGCCATCACCATC	120
Db	84690	ATTTCTTGTCTCTTCTTCCATCCTTCACGGGAGTGTGTGCACCCCTGGCTATCACCATC	84631
QY	121	TGAGATTTGAAGCCT	135
Db	84630	TGAGGTTAGGACCT	84616

RESULT 14
HUAC003108
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE

HUAC003108 164564 bp DNA linear PRI 23-NOV-1999
Human Chromosome 16 BAC clone C17987SK-327024, complete sequence.
AC003108
AC003108.1 GI:2833632
HTG.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 164564)
Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R.,
Fuhmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S.,
Eichler,E.E., Harris,P.C., Venier,J.C. and Adams,M.D.
Genome duplications and other features in 12 Mb of DNA sequence
from human chromosome 16p and 16q
Genomics 60 (3), 295-308 (1999)
99425270

PUBMED	10493829
REFERENCE	2 (bases 1 to 164564)
AUTHORS	Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
TITLE	Human Chromosome 16 BAC clone CIT987SK-327024
JOURNAL	unpublished
REFERENCE	3 (bases 1 to 164564)
AUTHORS	Adams,M.D. and Loftus,B.J.
TITLE	Direct Submission
JOURNAL	Submitted (19-NOV-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, Email: bjloftus@tigr.org
REFERENCE	4 (bases 1 to 164564)
AUTHORS	Adams,M.D.
TITLE	Direct Submission
JOURNAL	Submitted (05-FEB-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
REFERENCE	5 (bases 1 to 164564)
AUTHORS	Adams,M.D. and Loftus,B.J.
TITLE	Direct Submission
JOURNAL	Submitted (17-MAR-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
COMMENT	On Feb 5, 1998 this sequence version replaced gi:2827780. Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA e-mail address: mdadams@tigr.org. The orientation of the sequence is from Sp6 end to T7 end. Genes were identified by a combination of five methods including: XGRail (available by anonymous ftp from arthur.epm.ornl.gov), GeneFinder (Phil Green, University of Washington), Genscan (Chris Burge, http://genomic.stanford.edu/~chris/GENSCANW.html) searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi.hg1.html). Genes without pepetide homology having spliced EST hits are termed 'unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
FEATURES	Location/Qualifiers
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gene	28025..29390 /note="presence of CpG island"
mRNA	32335..60015 /gene="327024.2"
misc_feature	join(32335..32477,34498..34638,39032..39160,42555..44202,47273..47403,48499..48676,49233..49372,49490..49606,51409..51510,51706..51822,52429..52502,53024..53086,

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PINACELSPRKEQAMDLIIDDTENTNPEIMPKLPIDLGAHCSSKYVGKNISEVK
EDVVLGKSNQVCOSSGNHLENKVTGHLYVEQLTSDRGAHINSTCAAMPKLTHERY
ASSOCIASPNGTVSGLKPASMLEKNCLSOTLETNKSYDVKNPSPILLMQNONTRQOMDT
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Best Local Similarity    99.1%; Pred. No. 4,7e-18;
Matches 106; Conservative    0; Mismatches    1; Indels    0; Gaps    0;

QY     377 ATGAGGGCGAAGATAATGTCTCCTGATAGAAAATTGATCAAGCTGCAGGATATGAGA 436
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DB     1198 AGGAGGGCGCAAAGATAAATGTCTCCTGATAGAAAATTGATCAAGCTGCAGGATATGAGA 1257

QY     437 AGAAGCAAAACCACACTCTGTTCTGAAAAAGAGAGAGGTGGAG 483
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DB     1258 AGAAAGCAAAACCCGACCTCACTTGTCTTGAAAGAGAGAGGTGGAG 1304

RESULT 15
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LOCUS               AB002405 Homo sapiens mRNA for LAK-4p, complete cds.
VERSION              AB002405.2 GI:7209573
KEYWORDS              LAK-4p.
SOURCE                Homo sapiens male lymphoid mILr expressing LAK cell CDNA to mRNA.
ORGANISM              Homo sapiens
REFERENCE              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS              Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE                 1 (bases 1 to 1639)
                     Abe,Y. and Takaoka,Y.
REFERENCE              LAK-4 clone from the membrane lymphotoxin expressing subtraction
AUTHORS              library
TITLE                 Published Only in Database (1998)
JOURNAL REFERENCE    2 (bases 1 to 1639)
AUTHORS              Abe,Y. and Takaoka,Y.
TITLE                 Direct Submission
JOURNAL TITLE         Submitted (28-MAR-1997) Yasuhito Abe, Ehime University School of
                      Medicine, The Second Department of Surgery; Shigenobu, Onsen-gun,
                      Ehime 791-02, Japan (E-mail:yasuhito@ehime-u.ac.jp,
                      Tel:+81-89-964-5111, Fax:+81-89-960-5334)
COMMENT              On Mar 8, 2000 this sequence version replaced gi:2760120.
FEATURES              Sequence updated (05-Jan-1998)
                      Location/Qualifiers
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53.1387
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CDS

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VWVRHLEAGPRVSNLPMVHRILMENTFEVLSALLAVIYLNIOVVRGQKVICLL
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polya_site 1614
BASE COUNT 294 a 495 c 517 g 333 t
ORIGIN
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Query Match 17.6%; Score 100.4; DB 9; Length 1639;
Best Local Similarity 52.6%; Pred. No. 6.6e-17;
Matches 243; Conservative 0; Mismatches 216; Indels 3; Gaps 1;
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QY 2 TGATGAATTCACGCTCCGAGCAAGCCCTGGCGGCTCACAGATGATGACTTCTTCA 61
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Db 867 TGGCCAACTGCCAGCGCGCGCGGCTGCTGCTGCTCACAGATGAGCAGCTTCC 926

QY 62 TCTTCTGCTCTTTTCCACTTTTCACTGACCGGGCTTGTGACACCTGGCCATCACCATCT 121
   || || || || || || || || || || || || || || || || || || ||
Db 927 TCACGCTGCTCTGCTTCCCGCTTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCT 986

QY 122 GGAGATTGAAGCCTTCAGCTGAGTGGGCCCTTTTCGAGGCTGCTGCTCTTCATTCACT 181
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Db 987 GGCAGGTGAAGCCTTCAGGACCTGCGGCCCTTCCGAGCCTGACACCATGACGAGG 1046

QY 182 CCATCTACAGCTGATGACACCT--AAGTACAGGCTGCTGCTGCTGCTGCTGCTT 238
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Db 1047 CCGGCAAGGCTGTGGGTGCGCCACCTGAGAGCGGCGCAGGCCAGGGGTCTGCTGCTG 1106

QY 239 GGATCTATCGGAACCTCATTTGAGAGTGTGACATCTTTTCATCTCACCCTCATTTGTC 298
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Db 1107 GGGTGCACCGGTACTGATGAAACACCTTCTTGTCTTCTGCTGCTGCTGCTGCTG 1166

QY 299 TAAATCATCACTATCTTACTGCGAGATCACAGAGGGAAGAGATTAATGATAGGCTGC 358
   || || || || || || || || || || || || || || || || || || ||
Db 1167 TGGCCGTGATCTACTCAACATCCAGGTGTGCGGGGCCAGCGCAAGTCACTGCTGC 1226

QY 359 TCCATGAGCAGATCAATTAATGAGGCAAGATAAATGTTCTGATAGAAAATTTGATCA 418
   || || || || || || || || || || || || || || || || || || ||
Db 1227 TCAAGAGAGATGAGCAATGAGGAGGAGCAAAATCTTCTTAATCAACAAGCTTCACT 1286

QY 419 AGCTGAGATATGAGAGAAAGCAAAACCCAGCTCACTTG 460
   || || || || || || || || || || || || || || || || || || ||
Db 1287 CCATCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGTTG 1328
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